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**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/232,522**

OIPE

INPUT SET: S30384.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Hoffmann-La Roche Inc.
- (B) STREET: 340 Kingsland Street
- (C) CITY: Nutley
- (D) STATE: New Jersey
- (E) COUNTRY: United States
- (F) ZIP: 07110-1199

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Buchholz, Briana C.
(B) REGISTRATION NUMBER: 39,123
(C) REFERENCE/DOCKET NUMBER: CD 1048P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 973-235-6208
(B) TELEFAX: 973-235-2363

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

ENTERED

TC 1600 MAIL ROOM

JUL 19 1990

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PATENT APPLICATION US/09/232,522**

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47 (D) TOPOLOGY: linear
 48
 49 (ii) MOLECULE TYPE: cDNA
 50
 51 (iii) HYPOTHETICAL: NO
 52
 53 (iv) ANTI-SENSE: NO
 54
 55 (vi) ORIGINAL SOURCE:
 56 (A) ORGANISM: mouse
 57 (G) CELL TYPE: Hybridoma
 58 (H) CELL LINE: HIL-12F3-16G2
 59
 60 (ix) FEATURE:
 61 (A) NAME/KEY: CDS
 62 (B) LOCATION: 1..321
 63
 64
 65

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

68 CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC	48
69 Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser	
70 1 5 10 15	
72 CTC ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC	96
73 Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn	
74 20 25 30	
76 TGG ATC CGG AAA TTC CCA GGG AAT AAA TTT GAG TAC ATG GGA TTC ATA	144
77 Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile	
78 35 40 45	
80 AGT TAT AGT GGT AGC ACT TAC AAT AAT CCA TCT CTC AAA AAT CGA GTC	192
81 Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val	
82 50 55 60	
84 TCC ATC ACT CGA GAC ACA TCC AAT AAC CAG TAC TAC CTG CAG TTG AGT	240
85 Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser	
86 65 70 75 80	
88 TCT GTG ACT ACT GAG GAC TCA GCC ACA TAT TAC TGT GCA AGA TCT TCG	288
89 Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser	
90 85 90 95	
92 GAT GCT TTG GAC TAC TGG GGC GCA GGG ACC ACG	321
93 Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr	
94 100 105	

95
 96
 97 (2) INFORMATION FOR SEQ ID NO:2:

98
 99 (i) SEQUENCE CHARACTERISTICS:

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100 (A) LENGTH: 107 amino acids
101 (B) TYPE: amino acid
102 (D) TOPOLOGY: linear
103
104 (ii) MOLECULE TYPE: protein
105
106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
107
108 Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
109 1 5 10 15
110
111 Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn
112 20 25 30
113
114 Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile
115 35 40 45
116
117 Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
118 50 55 60
119
120 Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser
121 65 70 75 80
122
123 Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser
124 85 90 95
125
126 Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
127 100 105
128
129 (2) INFORMATION FOR SEQ ID NO:3:
130
131 (i) SEQUENCE CHARACTERISTICS:
132 (A) LENGTH: 308 base pairs
133 (B) TYPE: nucleic acid
134 (C) STRANDEDNESS: double
135 (D) TOPOLOGY: linear
136
137 (ii) MOLECULE TYPE: cDNA
138
139 (iii) HYPOTHETICAL: NO
140
141 (iv) ANTI-SENSE: NO
142
143 (vi) ORIGINAL SOURCE:
144 (A) ORGANISM: mouse
145 (G) CELL TYPE: Hybridoma
146 (H) CELL LINE: HIL-12F3-20E11
147
148 (ix) FEATURE:
149 (A) NAME/KEY: CDS
150 (B) LOCATION: 1..306
151
152

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153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

154

155 GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC	48
156 Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu	
157 1 5 10 15	
158	
159 ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG	96
160 Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp	
161 20 25 30	
162	
163 ATC CGG AAA TTC CCA GAT AAT ACA CTT GAG TAC ATG GGA TAC ATA AGT	144
164 Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser	
165 35 40 45	
166	
167 TAC AGT GGT AGT ACT TAC TAC AAT CCA TCT CTC AGA AGT CGA ATC TCC	192
168 Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser	
169 50 55 60	
170	
171 ATC ACT CGA GAC ACA TCC AAG AAC CAG TAC TCC ATG CAG TTG AAT TCT	240
172 Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser	
173 65 70 75 80	
174	
175 GTG ACT ACT GAG GAC ACA GCC ACA TAT TAC TGT GCA AGA TCC TCG GAT	288
176 Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp	
177 85 90 95	
178	
179 GCT ATG GAC TAC TGG GGC GC	308
180 Ala Met Asp Tyr Trp Gly	
181 100	
182	
183	
184 (2) INFORMATION FOR SEQ ID NO:4:	
185	
186 (i) SEQUENCE CHARACTERISTICS:	
187 (A) LENGTH: 102 amino acids	
188 (B) TYPE: amino acid	
189 (D) TOPOLOGY: linear	
190	
191 (ii) MOLECULE TYPE: protein	
192	
193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
194	
195 Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu	
196 1 5 10 15	
197	
198 Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp	
199 20 25 30	
200	
201 Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser	
202 35 40 45	
203	
204 Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser	
205 50 55 60	

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206
207 Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser
208 65 70 75 80
209
210 Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp
211 85 90 95
212
213 Ala Met Asp Tyr Trp Gly
214 100
215

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